

SEQUENCE LISTING

Kato, Kou

Yamada, Yasuhiro

Nihira, Takuya

Shindo, Takuya

<120> METHOD FOR INDUCTION OF GENE EXPRESSION IN PLANT AND PLANT TREATED THEREBY

<130> 5405/18

<140> 10/049,710

<141> 2002-02-15

<150> PCT/JP01/05096

<151> 2001-06-15

<150> JP 2000-180466

<151> 2000-06-15

<160> 11

<170> PatentIn version 3.1

<210> 1

<211> 699

<212> DNA

<213> Streptomyces virginiae

<220>

<221> CDS

<222> (1)..(699)

<223>

96

```
<300>
<301> Okamoto, S., Nakamura, K., Nihira, T. and Yamada, Y.
<302> Virginiae butanolide binding protein from Streptomyces virginiae.
Evidence that VbrA is not the virginiae butanolide binding protein and re-
identification of the true binding protein
      Journal of Biological Chemistry
<303>
<304>
       270
<305>
       20
<306>
       12319-12326
       1995-05-19
<307>
<308>
       D32251
<309>
       1994-07-19
<313>
      (1)..(699)
<300>
<301>
       Okamoto, S., Nakamura, K., Nihira, T. and Yamada, Y.
<302> Virginiae butanolide binding protein from Streptomyces virginiae.
Evidence that VbrA is not the virginiae butanolide binding protein and re-
identification of the true binding protein
       Journal of Biological Chemistry
<303>
<304>
       270
<305>
       20
<306>
      12319-12326
<307>
       1995-05-19
<308>
      D32251
<309>
       1994-07-19
<400> 1
atg gca gtg cga cac gaa cgg gtg gca gtg cga cag gaa cgg gcc gtc
                                                                       48
Met Ala Val Arg His Glu Arg Val Ala Val Arg Gln Glu Arg Ala Val
```

10

cgc acg cgg cag gcg atc gtg cgg gca gcc gcc tcg gtc ttc gac gag

Arg	Thr	Arg	Gln 20	Ala	Ile	Val	Arg	Ala 25	Ala	Ala	Ser	Val	Phe 30	Asp	Glu	
tac Tyr	ggg Gly	ttc Phe 35	gag Glu	gcc Ala	gcc Ala	aca Thr	gtg Val 40	gca Ala	gag Glu	atc Ile	ctc Leu	tcg Ser 45	cgg Arg	gcc Ala	tcg Ser	144
gtc Val	acc Thr 50	aag Lys	ggc Gly	gcg Ala	atg Met	tac Tyr 55	ttc Phe	cac His	ttc Phe	gct Ala	tcc Ser 60	aag Lys	gaa Glu	gag Glu	ctg Leu	192
gcc Ala 65	cgc Arg	ggc Gly	gtg Val	ctg Leu	gcc Ala 70	gag Glu	cag Gln	acc Thr	ctg Leu	cac His 75	gtg Val	gcg Ala	gtg Val	ccg Pro	gaa Glu 80	240
tcc Ser	ggc Gly	tcc Ser	aag Lys	gcg Ala 85	cag Gln	gaa Glu	ctg Leu	gta Val	gac Asp 90	ctc Leu	acc Thr	atg Met	ctg Leu	gtc Val 95	gcc Ala	288
cac His	ggc Gly	atg Met	ctg Leu 100	cac His	gat Asp	ccg Pro	atc Ile	ctg Leu 105	cgg Arg	gcg Ala	ggc Gly	acg Thr	cgg Arg 110	ctc Leu	gca Ala	336
ctg Leu	gac Asp	cag Gln 115	ggg	gcg Ala	gtg Val	gac Asp	ttc Phe 120	tcc Ser	gac Asp	gcc Ala	aac Asn	ccg Pro 125	ttc Phe	ggc	gag Glu	384
tgg Trp	ggc Gly 130	Asp	atc Ile	tgc Cys	gcc Ala	cag Gln 135	ctc Leu	ctg Leu	gcg Ala	gag Glu	gca Ala 140	cag Gln	gaa Glu	cgg Arg	ggg Gly	432
gag Glu 145	Val	ctt Leu	ccg Pro	cac His	gtg Val 150	Asn	ccg Pro	aaa Lys	aag Lys	acc Thr 155	Gly	gac Asp	ttc Phe	atc Ile	gtc Val 160	480
ggc Gly	tgc Cys	ttc Phe	acc Thr	ggg Gly 165	Leu	cag Gln	gcg Ala	gto Val	tcc Ser 170	Arg	gto Val	acc Thr	tcc Ser	gac Asp 175	cgc Arg	528
cag Gln	gac Asp	cto Leu	ggc Gly 180	His	cgg Arg	atc Ile	tcg Ser	gtg Val 185	. Met	tgg Trp	aac Asr	cac n His	gtg Val 190	Leu	ccc Pro	576
ago Ser	ato Ile	gtg Val	. Pro	gcg Ala	tcc Ser	atg Met	Leu 200	ı Thr	tgç Trp	g ato o Ile	gaa Glu	a acc a Thr 205	: Gl	gaç Glu	gag Glu	624
cgo Aro	g ato g Ile 210	e Gly	g aag 7 Lys	g gto Val	gcç Alá	g gcg Ala 215	Ala	g gco a Ala	c gaç a Glu	g gco ı Ala	e geo a Ala 220	a Glu	g gct ı Ala	gco Ala	g gag Glu	672
gcc Ala 22!	a Se	e gaq c Gli	g gco ı Ala	e geo a Ala	c tco a Sei 230	Asp	gaç Glı	g tag	3							699

<210> 2

<211> 232

<212> PRT

<213> Streptomyces virginiae

<400> 2

Met Ala Val Arg His Glu Arg Val Ala Val Arg Gln Glu Arg Ala Val 1 5 10 15

Arg Thr Arg Gln Ala Ile Val Arg Ala Ala Ala Ser Val Phe Asp Glu 20 25 30

Tyr Gly Phe Glu Ala Ala Thr Val Ala Glu Ile Leu Ser Arg Ala Ser 35 40 45

Val Thr Lys Gly Ala Met Tyr Phe His Phe Ala Ser Lys Glu Glu Leu 50 55 60

Ala Arg Gly Val Leu Ala Glu Gln Thr Leu His Val Ala Val Pro Glu 65 70 75 80

Ser Gly Ser Lys Ala Gln Glu Leu Val Asp Leu Thr Met Leu Val Ala 85 90 95

His Gly Met Leu His Asp Pro Ile Leu Arg Ala Gly Thr Arg Leu Ala 100 105 110

Leu Asp Gln Gly Ala Val Asp Phe Ser Asp Ala Asn Pro Phe Gly Glu 115 120 125

Trp Gly Asp Ile Cys Ala Gln Leu Leu Ala Glu Ala Gln Glu Arg Gly 130 135 140

Glu Val Leu Pro His Val Asn Pro Lys Lys Thr Gly Asp Phe Ile Val 145 150 155 160

Gly Cys Phe Thr Gly Leu Gln Ala Val Ser Arg Val Thr Ser Asp Arg 165 170 175

Gln Asp Leu Gly His Arg Ile Ser Val Met Trp Asn His Val Leu Pro 180 185 190

Ser Ile Val Pro Ala Ser Met Leu Thr Trp Ile Glu Thr Gly Glu Glu 195 200 205

Arg Ile Gly Lys Val Ala Ala Ala Glu Ala Ala Glu Ala Glu 210 215 220

Ala Ser Glu Ala Ala Ser Asp Glu 225 230

<210> 3

<211> 26

<212> DNA

<213> Streptomyces virginiae

<300>

<301> Kinoshita, H., Tsuji, T., Ipposhi, H., Nihira, T. and Yamada, Y.

<302> Characterization of Binding Sequences for Butyrolactone Autoregulator Receptors in Streptomycetes

<303> Journal of Bacteriology

<304> 181

<305> 16

<306> 5075-5080

<307> 1999-08

<308> D32251

<309> 1994-07-19

<313> (1)..(26)

<300>

<301> Kinoshita, H., Tsuji, T., Ipposhi, H., Nihira, T. and Yamada, Y.

<302> Characterization of Binding Sequences for Butyrolactone Autoregulator Receptors in Streptomycetes <303> Journal of Bacteriology <304> 181 <305> 16 <306> 5075-5080 <307> 1999-08 <308> D32251 <309> 1994-07-19 <400> 3 26 agatacatac caaccggttc ttttga <210> 4 <211> 110 <212> DNA <213> Artificial sequence <220> <223> Designed sequence of the CamV 35S promoter modified to contain the operator BARE-3 element just downstream of its TAT-box <400> -4 gatateteca etgacgtaag ggatgacgca caateecact ateettegea agaceettee 60 tctatataag agatacatac caaccggttc ttttgacggg ggactctaga 110 <210> 5 <211> 110

<212> DNA

60

110

<213> Artificial sequence <220> <223> Designed sequence of the CaMV 35S promoter modified to contain the operator BARE-3 element just upstream of its TATA-box <400> 5 gatateteca etgaegtaag ggatgaegea caateagata cataceaace ggttettttg actatataag gaagttcatt tcatttggag agaacacggg ggactctaga <210> 6

<211> 110

<212> DNA

<213> Artificial sequence

<220>

<223> Designed sequence of the CaMV 35S promoter modified to contain the operator BARE-3 elements just downstream and upstream of its TATA-box

<400> 6

gatateteca etgaegtaag ggatgaegea caateagata eataceaace ggttettttg 60 110 actatataag agatacatac caaccggttc ttttgacggg ggactctaga

<210> 7

<211> 136

<212> DNA

<213> Artificial sequence

<220>

<223> Designed sequence of the CaMV 35S promoter modified to contain three of the operator BARE-3 elements just downstream and upstream of its TATA-box

<400> 7

gatateteea etgaegtaag ggatgaegea eaateagata eataceaace ggttetttt 60 actatataag agatacatae eaaceggtte ttttgaagat acataceaac eggttetttt 120 gaegggggae tetaga 136

<210> 8

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> Designed sequence of a backward primer containing the restriction enzyme BamH I recognition sequence for PCR amplification of the barA gene coding region to be cloned by cut with the enzyme

<400> 8

taggatccat aaatggcagt gcgacac

27

<210> 9

<211> 27

<212> DNA

<213> Artificial sequence

<220>

 $<\!223\!>$ Designed sequence of a forward primer containing the restriction enzyme Sac Irecognition sequence for PCR amplification of the barA gene coding region to be cloned by cut with the enzyme

<400> 9

tagageteet actegtegga ggeggee

27

<210> 10

89

<211> 67 <212> DNA <213> Artificial sequence <220> <223> Designed sequence of one of paired oligo DNAs for construction of the modified CaMV 35S promoter containing three of the operator BARE-3 elements just downstream and upstream of its TATA-box <400> 10 cggatatctc cactgacgta agggatgacg cacaatcaga tacataccaa ccggttcttt 60 67 tgactat 11 <210> <211> 89 <212> DNA <213> Artificial sequence <220> <223> Designed sequence of the other of paired oligo DNAs for construction of the modified CaMV 35S promoter containing three of the operator BARE-3 elements just downstream and upstream of its TATA-box <400> 11 gctctagagt cccccgtcaa aagaaccggt tggtatgtat cttcaaaaga accggttggt 60

atgtatctct tatatagtca aaagaaccg